CRF Problem Report

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Application Serial Number: C9 /841,720 C

Filing Date: 4-24-2001

Date Processed by STIC: 6-14-02

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JUL 0 8 2002

STIC Contact: **Mark Spencer, 703-308-4212**

TECH CENTER 1600/2900

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Revised 01/29/2002

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10/09   OIPE

RAW SEQUENCE LISTING   DATE: 06/14/2001
PATENT APPLICATION: US/09/841,720   TIME: 15:43:26

Input Set : N:\Crf3\RULE60\09841720.txt
Output Set: N:\CRF3\06142001\I841720.raw

SEQUENCE LISTING
```
 3 (1) GENERAL INFORMATION:
 5       (i) APPLICANT: Yu, Lei
 7      (ii) TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSOTIONS AND
 8                              METHODS
10     (iii) NUMBER OF SEQUENCES: 9
12      (iv) CORRESPONDENCE ADDRESS:
13           (A) ADDRESSEE: Arnold, White & Durkee
14           (B) STREET: P.O. Box 4433
15           (C) CITY: Houston
16           (D) STATE: Texas
17           (E) COUNTRY: USA
18           (F) ZIP: 77210
20       (v) COMPUTER READABLE FORM:
21           (A) MEDIUM TYPE: Floppy disk
22           (B) COMPUTER: IBM PC compatible
23           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26      (vi) CURRENT APPLICATION DATA:
C--> 27           (A) APPLICATION NUMBER: US/09/841,720
C--> 28           (B) FILING DATE: 24-Apr-2001
29           (C) CLASSIFICATION:
31     (vii) PRIOR APPLICATION DATA:
32           (A) APPLICATION NUMBER: 08/120,601
33           (B) FILING DATE: 13-SEP-1993
36    (viii) ATTORNEY/AGENT INFORMATION:
37           (A) NAME: Wilson, Mark B.
38           (B) REGISTRATION NUMBER: 37,259
39           (C) REFERENCE/DOCKET NUMBER: INDA:002
41      (ix) TELECOMMUNICATION INFORMATION:
42           (A) TELEPHONE: 512/418-3000
43           (B) TELEFAX: 512/474-7577
46 (2) INFORMATION FOR SEQ ID NO: 1:
48       (i) SEQUENCE CHARACTERISTICS:
49           (A) LENGTH: 1618 base pairs
50           (B) TYPE: nucleic acid
51           (C) STRANDEDNESS: single
52           (D) TOPOLOGY: linear
55      (ix) FEATURE:
56           (A) NAME/KEY: CDS
57           (B) LOCATION: 214..1407
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
62 CGTGGAAGGG GGCTACAAGC AGAGGAGAAT ATCAGACGCT CAGACGTTCC CTTCTGCCTG      60
64 CCGCTCTTCT CTGGTTCCAC TAGGGCTGGT CCATGTAAGA ATCTGACGGA GCCTAGGGCA     120
66 GCTGTGAGAG GAAGAGGCTG GGGCGCGTGG AACCCGAAAA GTCTGAGTGC TCTCAGTTAC     180
68 AGCCTACCTA GTCCGCAGCA GGCCTTCAGC ACC ATG GAC AGC AGC ACC GGC CCA     234
69                                     Met Asp Ser Ser Thr Gly Pro
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70                                           1              5
72 GGG AAC ACC AGC GAC TGC TCA GAC CCC TTA GCT CAG GCA AGT TGC TCC       282
73 Gly Asn Thr Ser Asp Cys Ser Asp Pro Leu Ala Gln Ala Ser Cys Ser
74           10                  15                  20
76 CCA GCA CCT GGC TCC TGG CTC AAC TTG TCC CAC GTT GAT GGC AAC CAG       330
77 Pro Ala Pro Gly Ser Trp Leu Asn Leu Ser His Val Asp Gly Asn Gln
78      25                  30                  35
80 TCC GAT CCA TGC GGT CTG AAC CGC ACC GGG CTT GGC GGG AAC GAC AGC       378
81 Ser Asp Pro Cys Gly Leu Asn Arg Thr Gly Leu Gly Gly Asn Asp Ser
82  40                  45                  50                  55
84 CTG TGC CCT CAG ACC GGC AGC CCT TCC ATG GTC ACA GCC ATT ACC ATC       426
85 Leu Cys Pro Gln Thr Gly Ser Pro Ser Met Val Thr Ala Ile Thr Ile
86                  60                  65                  70
88 ATG GCC CTC TAC TCT ATC GTG TGT GTA GTG GGC CTC TTC GGA AAC TTC       474
89 Met Ala Leu Tyr Ser Ile Val Cys Val Val Gly Leu Phe Gly Asn Phe
90              75                  80                  85
92 CTG GTC ATG TAT GTG ATT GTA AGA TAC ACC AAA ATG AAG ACT GCC ACC       522
93 Leu Val Met Tyr Val Ile Val Arg Tyr Thr Lys Met Lys Thr Ala Thr
94          90                  95                  100
96 AAC ATC TAC ATT TTC AAC CTT GCT CTG GCA GAC GCC TTA GCG ACC AGT       570
97 Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu Ala Thr Ser
98      105                 110                 115
100 ACA CTG CCC TTT CAG AGT GTC AAC TAC CTG ATG GGA ACA TGG CCC TTC      618
101 Thr Leu Pro Phe Gln Ser Val Asn Tyr Leu Met Gly Thr Trp Pro Phe
102 120                 125                 130                 135
104 GGA ACC ATC CTC TGC AAG ATC GTG ATC TCA ATA GAT TAC TAC AAC ATG      666
105 Gly Thr Ile Leu Cys Lys Ile Val Ile Ser Ile Asp Tyr Tyr Asn Met
106                 140                 145                 150
108 TTC ACC AGC ATA TTC ACC CTC TGC ACC ATG AGC GTG GAC CGC TAC ATT      714
109 Phe Thr Ser Ile Phe Thr Leu Cys Thr Met Ser Val Asp Arg Tyr Ile
110                 155                 160                 165
112 GCT GTC TGC CAC CCA GTC AAA GCC CTG GAT TTC CGT ACC CCC CGA AAT      762
113 Ala Val Cys His Pro Val Lys Ala Leu Asp Phe Arg Thr Pro Arg Asn
114             170                 175                 180
116 GCC AAA ATC GTC AAC GTC TGC AAC TGG ATC CTC TCT TCT GCC ATC GGT      810
117 Ala Lys Ile Val Asn Val Cys Asn Trp Ile Leu Ser Ser Ala Ile Gly
118     185                 190                 195
120 CTG CCT GTA ATG TTC ATG GCA ACC ACA AAA TAC AGG CAG GGG TCC ATA      858
121 Leu Pro Val Met Phe Met Ala Thr Thr Lys Tyr Arg Gln Gly Ser Ile
122 200                 205                 210                 215
124 GAT TGC ACC CTC ACG TTC TCC CAC CCA ACC TGG TAC TGG GAG AAC CTG      906
125 Asp Cys Thr Leu Thr Phe Ser His Pro Thr Trp Tyr Trp Glu Asn Leu
126                 220                 225                 230
128 CTC AAA ATC TGT GTC TTT ATC TTC GCT TTC ATC ATG CCG ATC CTC ATC      954
129 Leu Lys Ile Cys Val Phe Ile Phe Ala Phe Ile Met Pro Ile Leu Ile
130                 235                 240                 245
132 ATC ACT GTG TGT TAC GGC CTG ATG ATC TTA CGA CTC AAG AGC GTT CGC      1002
133 Ile Thr Val Cys Tyr Gly Leu Met Ile Leu Arg Leu Lys Ser Val Arg
134         250                 255                 260
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```
136 ATG CTA TCG GGC TCC AAA GAA AAG GAC AGG AAT CTG CGC AGG ATC ACC      1050
137 Met Leu Ser Gly Ser Lys Glu Lys Asp Arg Asn Leu Arg Arg Ile Thr
138     265                 270                 275
140 CGG ATG GTG CTG GTG GTC GTG GCT GTA TTT ATC GTC TGC TGG ACC CCC      1098
141 Arg Met Val Leu Val Val Val Ala Val Phe Ile Val Cys Trp Thr Pro
142 280                 285                 290                 295
144 ATC CAC ATC TAC GTC ATC ATC AAA GCG CTG ATC ACG ATT CCA GAA ACC      1146
145 Ile His Ile Tyr Val Ile Ile Lys Ala Leu Ile Thr Ile Pro Glu Thr
146                 300                 305                 310
148 ACA TTT CAG ACC GTT TCC TGG CAC TTC TGC ATT GCT TTG GGT TAC ACG      1194
149 Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile Ala Leu Gly Tyr Thr
150     315                 320                 325
152 AAC AGC TGC CTG AAT CCA GTT CTT TAC GCC TTC CTG GAT GAA AAC TTC      1242
153 Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe
154     330                 335                 340
156 AAG CGA TGC TTC AGA GAG TTC TGC ATC CCA ACC TCG TCC ACG ATC GAA      1290
157 Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Thr Ile Glu
158     345                 350                 355
160 CAG CAA AAC TCC ACT CGA GTC CGT CAG AAC ACT AGG GAA CAT CCC TCC      1338
161 Gln Gln Asn Ser Thr Arg Val Arg Gln Asn Thr Arg Glu His Pro Ser
162 360                 365                 370                 375
164 ACG GCT AAT ACA GTG GAT CGA ACT AAC CAC CAG CTA GAA AAT CTG GAG      1386
165 Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Leu Glu Asn Leu Glu
166                 380                 385                 390
168 GCA GAA ACT GCT CCA TTG CCC TAACTGGGTC TCACACCATC CAGACCCTCG        1437
169 Ala Glu Thr Ala Pro Leu Pro
170                 395
172 CTAAGCTTAG AGGCCGCCAT CTACGTGGAA TCAGGTTGCT GTCAGGGTGT GTGGGAGGCT   1497
174 CTGGTTTCCT GAGAAACCAT CTGATCCTGC ATTCAAAGTC ATTCCTCTCT GGCTACTTCA   1557
176 CTCTGCACAT GAGAGATGCT CAGACTGATC AAGACCAGAA GAAAGAAGAG ACTACCGGAC   1617
178 A                                                                  1618
181 (2) INFORMATION FOR SEQ ID NO: 2:
183     (i) SEQUENCE CHARACTERISTICS:
184         (A) LENGTH: 398 amino acids
185         (B) TYPE: amino acid
186         (D) TOPOLOGY: linear
188     (ii) MOLECULE TYPE: protein
190     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
192 Met Asp Ser Ser Thr Gly Pro Gly Asn Thr Ser Asp Cys Ser Asp Pro
193 1                 5                 10                 15
195 Leu Ala Gln Ala Ser Cys Ser Pro Ala Pro Gly Ser Trp Leu Asn Leu
196             20                 25                 30
198 Ser His Val Asp Gly Asn Gln Ser Asp Pro Cys Gly Leu Asn Arg Thr
199         35                 40                 45
201 Gly Leu Gly Gly Asn Asp Ser Leu Cys Pro Gln Thr Gly Ser Pro Ser
202     50                 55                 60
204 Met Val Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val Cys Val
205 65                 70                 75                 80
207 Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val Arg Tyr
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```
208                85              90              95
210 Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu
211          100              105              110
213 Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val Asn Tyr
214          115              120              125
216 Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile Val Ile
217      130              135              140
219 Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Cys Thr
220 145              150              155              160
222 Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu
223              165              170              175
225 Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Val Asn Val Cys Asn Trp
226          180              185              190
228 Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala Thr Thr
229          195              200              205
231 Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser His Pro
232      210              215              220
234 Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile Phe Ala
235 225              230              235              240
237 Phe Ile Met Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Ile
238              245              250              255
240 Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu Lys Asp
241          260              265              270
243 Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val Ala Val
244          275              280              285
246 Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile Lys Ala
247      290              295              300
249 Leu Ile Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp His Phe
250 305              310              315              320
252 Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val Leu Tyr
253              325              330              335
255 Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe Cys Ile
256          340              345              350
258 Pro Thr Ser Ser Thr Ile Glu Gln Gln Asn Ser Thr Arg Val Arg Gln
259          355              360              365
261 Asn Thr Arg Glu His Pro Ser Thr Ala Asn Thr Val Asp Arg Thr Asn
262      370              375              380
264 His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
265 385              390              395
268 (2) INFORMATION FOR SEQ ID NO: 3:
270     (i) SEQUENCE CHARACTERISTICS:
271          (A) LENGTH: 1618 base pairs
272          (B) TYPE: nucleic acid
273          (C) STRANDEDNESS: single
274          (D) TOPOLOGY: linear
277     (ix) FEATURE:
278          (A) NAME/KEY: CDS
279          (B) LOCATION: 339..1232
282.    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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```
284 CGTGGAAGGG GGCTACAAGC AGAGGAGAAT ATCAGACGCT CAGACGTTCC CTTCTGCCTG          60
286 CCGCTCTTCT CTGGTTCCAC TAGGGCTGGT CCATGTAAGA ATCTGACGGA GCCTAGGGCA         120
288 GCTGTGAGAG GAAGAGGCTG GGGCGCGTGG AACCCGAAAA GTCTGAGTGC TCTCAGTTAC         180
290 AGCCTACCTA GTCCGCAGCA GGCCTTCAGC ACCATGGACA GCAGCACCGG CCCAGGGAAC         240
292 ACCAGCGACT GCTCAGACCC CTTAGCTCAG GCAAGTTGCT CCCCAGCACC TGGCTCCTGG         300
294 CTCAACTTGT CCCACGTTGA TGGCAACCAG TCCGATCC ATG CGG TCT GAA CCG           353
295                                             Met Arg Ser Glu Pro
296                                              1               5
298 CAC CGG GCT TGG CGG GAA CGA CAG CCT GTG CCC TCA GAC CGG CAG CCC         401
299 His Arg Ala Trp Arg Glu Arg Gln Pro Val Pro Ser Asp Arg Gln Pro
300              10                  15                  20
302 TTC CAT GGT CAC AGC CAT TAC CAT CAT GGC CCT CTA CTC TAT CGT GTG         449
303 Phe His Gly His Ser His Tyr His His Gly Pro Leu Leu Tyr Arg Val
304              25                  30                  35
306 TGT AGT GGG CCT CTT CGG AAA CTT CCT GGT CAT GTA TGT GAT TGT AAG         497
307 Cys Ser Gly Pro Leu Arg Lys Leu Pro Gly His Val Cys Asp Cys Lys
308              40                  45                  50
310 ATA CAC CAA AAT GAA GAC TGC CAC CAA CAT CTA CAT TTT CAA CCT TGC         545
311 Ile His Gln Asn Glu Asp Cys His Gln His Leu His Phe Gln Pro Cys
312     55                  60                  65
314 TCT GGC AGA CGC CTT AGC GAC CAG TAC ACT GCC CTT TCA GAG TGT CAA         593
315 Ser Gly Arg Arg Leu Ser Asp Gln Tyr Thr Ala Leu Ser Glu Cys Gln
316 70                  75                  80                  85
318 CTA CCT GAT GGG AAC ATG GCC CTT CGG AAC CAT CCT CTG CAA GAT CGT         641
319 Leu Pro Asp Gly Asn Met Ala Leu Arg Asn His Pro Leu Gln Asp Arg
320              90                  95                  100
322 GAT CTC AAT AGA TTA CTA CAA CAT GTT CAC CAG CAT ATT CAC CCT CTG         689
323 Asp Leu Asn Arg Leu Leu Gln His Val His Gln His Ile His Pro Leu
324              105                 110                 115
326 CAC CAT GAG CGT GGA CCG CTA CAT TGC TGT CTG CCA CCC AGT CAA AGC         737
327 His His Glu Arg Gly Pro Leu His Cys Cys Leu Pro Pro Ser Gln Ser
328              120                 125                 130
330 CCT GGA TTT CCG TAC CCC CCG AAA TGC CAA AAT CGT CAA CGT CTG CAA         785
331 Pro Gly Phe Pro Tyr Pro Pro Lys Cys Gln Asn Arg Gln Arg Leu Gln
332     135                 140                 145
334 CTG GAT CCT CTC TTC TGC CAT CGG TCT GCC TGT AAT GTT CAT GGC AAC         833
335 Leu Asp Pro Leu Phe Cys His Arg Ser Ala Cys Asn Val His Gly Asn
336 150                 155                 160                 165
338 CAC AAA ATA CAG GCA GGG GTC CAT AGA TTG CAC CCT CAC GTT CTC CCA         881
339 His Lys Ile Gln Ala Gly Val His Arg Leu His Pro His Val Leu Pro
340              170                 175                 180
342 CCC AAC CTG GTA CTG GGA GAA CCT GCT CAA AAT CTG TGT CTT TAT CTT         929
343 Pro Asn Leu Val Leu Gly Glu Pro Ala Gln Asn Leu Cys Leu Tyr Leu
344              185                 190                 195
346 CGC TTT CAT CAT GCC GAT CCT CAT CAT CAC TGT GTG TTA CGG CCT GAT         977
347 Arg Phe His His Ala Asp Pro His His His Cys Val Leu Arg Pro Asp
348     200                 205                 210
350 GAT CTT ACG ACT CAA GAG CGT TCG CAT GCT ATC GGG CTC CAA AGA AAA        1025
351 Asp Leu Thr Thr Gln Glu Arg Ser His Ala Ile Gly Leu Gln Arg Lys
```

VERIFICATION SUMMARY   DATE: 06/14/2001
PATENT APPLICATION: **US/09/841,720**   TIME: 15:43:27

Input Set : **N:\Crf3\RULE60\09841720.txt**
Output Set: **N:\CRF3\06142001\I841720.raw**

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]